

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/643,434A

Source: 1FW16

Date Processed by STIC: 8/15/05

ENTERED



IFW16

RAW SEQUENCE LISTING DATE: 08/15/2005
 PATENT APPLICATION: US/10/643,434A TIME: 08:23:48

Input Set : A:\00786.366003.seqlist.txt
 Output Set: N:\CRF4\08152005\J643434A.raw

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3 <110> APPLICANT: Sheen, Jen
4      Kovtun, Yelena
5      Chiu, Wan-Ling
7 <120> TITLE OF INVENTION: Transgenic Plants Expressing a MAPKKK Protein Kinase Domain
9 <130> FILE REFERENCE: 00786/366003
11 <140> CURRENT APPLICATION NUMBER: 10/643,434A
C--> 12 <141> CURRENT FILING DATE: 2003-09-19
14 <150> PRIOR APPLICATION NUMBER: 09/371,338
15 <151> PRIOR FILING DATE: 1999-08-10
17 <150> PRIOR APPLICATION NUMBER: 60/095,938
18 <151> PRIOR FILING DATE: 1998-08-10
20 <160> NUMBER OF SEQ ID NOS: 24
22 <170> SOFTWARE: PatentIn version 3.3
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25 <211> LENGTH: 21
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Oligonucleotide Primer
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61 <211> LENGTH: 29
62 <212> TYPE: DNA
63 <213> ORGANISM: Artificial Sequence
65 <220> FEATURE:
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75 <213> ORGANISM: Artificial Sequence
77 <220> FEATURE:
78 <223> OTHER INFORMATION: Oligonucleotide Primer
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87 <213> ORGANISM: Artificial Sequence
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97 <211> LENGTH: 661
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99 <213> ORGANISM: Arabidopsis thaliana
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107 Asn Gln Glu Asn Gln Pro Pro Phe Pro Gly Val Leu Ala Asp Lys Ile
108          20          25          30
111 Thr Ser Cys Ile Arg Lys Ser Lys Ile Phe Ile Lys Pro Ser Phe Ser
112          35          40          45
115 Pro Pro Pro Pro Ala Asn Thr Val Asp Met Ala Pro Pro Ile Ser Trp
116          50          55          60
119 Arg Lys Gly Gln Leu Ile Gly Arg Gly Ala Phe Gly Thr Val Tyr Met
120 65          70          75          80
123 Gly Met Asn Leu Asp Ser Gly Glu Leu Leu Ala Val Lys Gln Val Leu
124          85          90          95
127 Ile Ala Ala Asn Phe Ala Ser Lys Glu Lys Thr Gln Ala His Ile Gln
128          100         105         110
131 Glu Leu Glu Glu Glu Val Lys Leu Leu Lys Asn Leu Ser His Pro Asn
132          115         120         125
135 Ile Val Arg Tyr Leu Gly Thr Val Arg Glu Asp Asp Thr Leu Asn Ile
136          130         135         140
139 Leu Leu Glu Phe Val Pro Gly Gly Ser Ile Ser Ser Leu Leu Glu Lys
140 145          150         155         160
143 Phe Gly Pro Phe Pro Glu Ser Val Val Arg Thr Tyr Thr Arg Gln Leu
144          165         170         175
147 Leu Leu Gly Leu Glu Tyr Leu His Asn His Ala Ile Met His Arg Asp
148          180         185         190
151 Ile Lys Gly Ala Asn Ile Leu Val Asp Asn Lys Gly Cys Ile Lys Leu
152          195         200         205

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155 Ala Asp Phe Gly Ala Ser Lys Gln Val Ala Glu Leu Ala Thr Met Thr
156      210                      215                      220
159 Gly Ala Lys Ser Met Lys Gly Thr Pro Tyr Trp Met Ala Pro Glu Val
160 225                      230                      235                      240
163 Ile Leu Gln Thr Gly His Ser Phe Ser Ala Asp Ile Trp Ser Val Gly
164                      245                      250                      255
167 Cys Thr Val Ile Glu Met Val Thr Gly Lys Ala Pro Trp Ser Gln Gln
168                      260                      265                      270
171 Tyr Lys Glu Val Ala Ala Ile Phe Phe Ile Gly Thr Thr Lys Ser His
172                      275                      280                      285
175 Pro Pro Ile Pro Asp Thr Leu Ser Ser Asp Ala Lys Asp Phe Leu Leu
176      290                      295                      300
179 Lys Cys Leu Gln Glu Val Pro Asn Leu Arg Pro Thr Ala Ser Glu Leu
180 305                      310                      315                      320
183 Leu Lys His Pro Phe Val Met Gly Lys His Lys Glu Ser Ala Ser Thr
184                      325                      330                      335
187 Asp Leu Gly Ser Val Leu Asn Asn Leu Ser Thr Pro Leu Pro Leu Gln
188                      340                      345                      350
191 Ile Asn Asn Thr Lys Ser Thr Pro Asp Ser Thr Cys Asp Asp Val Gly
192                      355                      360                      365
195 Asp Met Cys Asn Phe Gly Ser Leu Asn Tyr Ser Leu Val Asp Pro Val
196      370                      375                      380
199 Lys Ser Ile Gln Asn Lys Asn Leu Trp Gln Gln Asn Asp Asn Gly Gly
200 385                      390                      395                      400
203 Asp Glu Asp Asp Met Cys Leu Ile Asp Asp Glu Asn Phe Leu Thr Phe
204                      405                      410                      415
207 Asp Gly Glu Met Ser Ser Thr Leu Glu Lys Asp Cys His Leu Lys Lys
208                      420                      425                      430
211 Ser Cys Asp Asp Ile Ser Asp Met Ser Ile Ala Leu Lys Ser Lys Phe
212                      435                      440                      445
215 Asp Glu Ser Pro Gly Asn Gly Glu Lys Glu Ser Thr Met Ser Met Glu
216      450                      455                      460
219 Cys Asp Gln Pro Ser Tyr Ser Glu Asp Asp Asp Glu Leu Thr Glu Ser
220 465                      470                      475                      480
223 Lys Ile Lys Ala Phe Leu Asp Glu Lys Ala Ala Asp Leu Lys Lys Leu
224                      485                      490                      495
227 Gln Thr Pro Leu Tyr Glu Glu Phe Tyr Asn Ser Leu Ile Thr Phe Ser
228                      500                      505                      510
231 Pro Ser Cys Met Glu Ser Asn Leu Ser Asn Ser Lys Arg Glu Asp Thr
232                      515                      520                      525
235 Ala Arg Gly Phe Leu Lys Leu Pro Pro Lys Ser Arg Ser Pro Ser Arg
236      530                      535                      540
239 Gly Pro Leu Gly Gly Ser Pro Ser Arg Ala Thr Asp Ala Thr Ser Cys
240 545                      550                      555                      560
243 Ser Lys Ser Pro Gly Ser Gly Gly Ser Arg Glu Leu Asn Ile Asn Asn
244                      565                      570                      575
247 Gly Gly Asp Glu Ala Ser Gln Asp Gly Val Ser Ala Arg Val Thr Asp
248                      580                      585                      590
251 Trp Arg Gly Leu Val Val Asp Thr Lys Gln Glu Leu Ser Gln Cys Val

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252          595          600          605
255 Ala Leu Ser Glu Ile Glu Lys Lys Trp Lys Glu Glu Leu Asp Gln Glu
256          610          615          620
259 Leu Glu Arg Lys Arg Gln Glu Ile Met Arg Gln Ala Gly Leu Gly Ser
260 625          630          635          640
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264          645          650          655
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272 <211> LENGTH: 2155
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274 <213> ORGANISM: Arabidopsis thaliana
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279 ccagcctccg tttcccgggtg ttctcgccga taagatcacc tcttgcatcc gcaaatcgaa      120
281 gattttttatc aaaccctcct tctcgctcct tcctcctgct aacactgtag acatggcacc      180
283 tccgattttcg tggaggaaaag gtcagttaat tggtcgcggc gcgtttggta cgggtgtacat      240
285 gggatatgaat cttgactccg gggagcttct cgccgtcaaa caggttctga ttgcagccaa      300
287 ttttgcttcc aaggaaaaaga ctcaggctca tattcaggag cttgaagaag aagttaagct      360
289 tcttaaaaaat ctctcccatc ctaatatagt tagatatattg ggtacagtga gggaagatga      420
291 taccctgaat atccttctcg agtttgcttc cggtggtatc atatcatcgc tcttgagaa      480
293 atttggaacct tttcctgaat cagttgtccg gacatacaca aggcaactgc ttttaggggt      540
295 ggagtacctg cacaatcatg caattatgca cagagacatt aaggggggcta atatccttgt      600
297 ggataataaaa ggatgcatta agcttgctga ttttggtgca tccaaacaag tagctgagtt      660
299 ggctacgatg actggtgcaa aatctatgaa agggacacca tattggatgg ctccggaagt      720
301 tatccttcaa actggacata gcttctctgc tgacatatgg agcgtcggct gtacagttat      780
303 tgaaatggtg actgggaagg ctccttgagg tcagcagtat aaagaggttg ctgctatctt      840
305 cttcatagga acaacaaaat cacatcctcc aatacctgat actctctcct ctgatgcaaa      900
307 agattttctg ctcaagtgtc tgcaggaggt accaaatctg cgccaaccg catctgagct      960
309 actaaagcat ccttttgta tggggaaaca caaggagctt gcttctactg atcttggttc      1020
311 tgtcctgaac aatcttagca ctccactacc gttacagata aataacacca agagcactcc      1080
313 agattctact tgcgacgatg taggtgacat gtgtaacttt ggcagtttga attattcact      1140
315 tgtagatcct gtgaaatcaa tccaaaacaa aaatttatgg caacaaaatg ataatggagg      1200
317 tgatgaagac gatatgtgtt tgatagatga tgagaatttc ttgacatttg acggagaaat      1260
319 gagttctacc cttgaaaaag attgtcatct gaagaagagc tgtgatgaca taagtgatat      1320
321 gtccattgct ttgaagtcca aatttgacga aagtcctggt aatggagaga aagagtctac      1380
323 aatgagcatg gaatgtgacc aaccttcata ctcagaggat gatgatgagc tgaccgagtc      1440
325 aaaaattaaa gctttcttag atgagaaggc tgcagatcta aagaagttac agactcctct      1500
327 ctatgaagaa ttctacaata gtttgatcac attctctccc agttgtatgg agagtaattt      1560
329 aagtaacagt aaaagagagg aactgtctcg tggtttcctg aaactgcctc caaaaagcag      1620
331 gtcaccgagt cggggccctc ttggtggttc accttcaaga gcaacagacg caactagttg      1680
333 ttccaagagc ccaggaagtg gaggtagtcg tgaattgaat attaacaatg gaggtgatga      1740
335 agcttcacag gatggtgtat cagcacgggt cacagactgg aggggcctcg ttgttgacac      1800
337 taagcaggaa ttaagccagt gtgttgcttt gtcagagata gagaagaagt ggaaggaaga      1860
339 gcttgatcaa gaactggaaa gaaagcgaca agaaatcatg cgccaagcag ggttgggatc      1920
341 atccccaaga gacagaggca tgagccgaca gagagagaag tcgaggtttg catcaccagg      1980
343 aaaatgactt gcacaaaaag tctccggctt tttgattttt gattgctcaa ctagtatata      2040
345 tatctgtaac tcttatctcg ctgtgatgaa aagtagacac gaggtttggt ctgaatatat      2100

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351 <211> LENGTH: 268
352 <212> TYPE: PRT
353 <213> ORGANISM: Arabidopsis thaliana
355 <400> SEQUENCE: 9
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362          20          25          30
365 Val Lys Gln Val Leu Ile Ala Ala Asn Phe Ala Ser Lys Glu Lys Thr
366          35          40          45
369 Gln Ala His Ile Gln Glu Leu Glu Glu Val Lys Leu Leu Lys Asn
370          50          55          60
373 Leu Ser His Pro Asn Ile Val Arg Tyr Leu Gly Thr Val Arg Glu Asp
374 65          70          75          80
377 Asp Thr Leu Asn Ile Leu Leu Glu Phe Val Pro Gly Gly Ser Ile Ser
378          85          90          95
381 Ser Leu Leu Glu Lys Phe Gly Pro Phe Pro Glu Ser Val Val Arg Thr
382          100         105         110
385 Tyr Thr Arg Gln Leu Leu Leu Gly Leu Glu Tyr Leu His Asn His Ala
386          115         120         125
389 Ile Met His Arg Asp Ile Lys Gly Ala Asn Ile Leu Val Asp Asn Lys
390          130         135         140
393 Gly Cys Ile Lys Leu Ala Asp Phe Gly Ala Ser Lys Gln Val Ala Glu
394 145         150         155         160
397 Leu Ala Thr Met Thr Gly Ala Lys Ser Met Lys Gly Thr Pro Tyr Trp
398          165         170         175
401 Met Ala Pro Glu Val Ile Leu Gln Thr Gly His Ser Phe Ser Ala Asp
402          180         185         190
405 Ile Trp Ser Val Gly Cys Thr Val Ile Glu Met Val Thr Gly Lys Ala
406          195         200         205
409 Pro Trp Ser Gln Gln Tyr Lys Glu Val Ala Ala Ile Phe Phe Ile Gly
410          210         215         220
413 Thr Thr Lys Ser His Pro Pro Ile Pro Asp Thr Leu Ser Ser Asp Ala
414 225         230         235         240
417 Lys Asp Phe Leu Leu Lys Cys Leu Gln Glu Val Pro Asn Leu Arg Pro
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426 <211> LENGTH: 802
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435 ttttgcttcc aaggaaaaga ctcaggctca tattcaggag cttgaagaag aagttaagct      180
437 tcttaaaaat ctctcccatc ctaatatagt tagatatttg ggtacagtga gggaagatga      240

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VERIFICATION SUMMARY

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